

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/501,611
Source: PCT
Date Processed by STIC: 11/18/2005

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

SUGGESTED CORRECTION

SERIAL NUMBER: 10/S 01, 611

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1** _____ Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2** _____ Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3** _____ Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4** _____ Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5** _____ Variable Length Sequence(s)_____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6** _____ PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7** _____ Skipped Sequences
 (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
- Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8** _____ Skipped Sequences
 (NEW RULES) Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9** _____ Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10** _____ Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11** _____ Use of <220> ~~Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.~~

Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12** _____ PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13** _____ Misuse of n/Xaa "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



P
PCT

RAW SEQUENCE LISTING

DATE: 11/18/2005

PATENT APPLICATION: US/10/501,611

TIME: 10:51:29

Input Set : A:\-148-1.app

Output Set: N:\CRF4\11182005\J501611.raw

3 <110> APPLICANT: Pavan, William J.
 4 Loftus, Stacie K.
 5 The Government of the United States of America
 6 as represented by The Secretary of the
 7 Department of Health and Human Services
 9 <120> TITLE OF INVENTION: Alteration of RAB38 Function to Modulate Mammalian
 10 Pigmentation
 12 <130> FILE REFERENCE: 015280-148100US
 14 <140> CURRENT APPLICATION NUMBER: US 10/501,611
 15 <141> CURRENT FILING DATE: 2004-07-14
 17 <150> PRIOR APPLICATION NUMBER: US 60/349,929
 18 <151> PRIOR FILING DATE: 2002-01-18
 20 <150> PRIOR APPLICATION NUMBER: WO PCT/US03/01622
 21 <151> PRIOR FILING DATE: 2003-01-17
 23 <160> NUMBER OF SEQ ID NOS: 28
 25 <170> SOFTWARE: PatentIn Ver. 2.1
 27 <210> SEQ ID NO: 1
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 29 <212> TYPE: DNA
 30 <213> ORGANISM: Mus musculus
 32 <220> FEATURE:
 33 <223> OTHER INFORMATION: Rab38 sequence of wildtype allele in C57Bl6/J +/-
 34 DNA
 36 <400> SEQUENCE: 1
 37 ctgggtgt 8
 40 <210> SEQ ID NO: 2
 41 <211> LENGTH: 8
 42 <212> TYPE: DNA
 43 <213> ORGANISM: Mus musculus
 45 <220> FEATURE:
 46 <223> OTHER INFORMATION: Rab38 sequence of chocolate (cht) mutant allele in
 47 c57Bl6/J Rab38cht/+ DNA
 49 <400> SEQUENCE: 2
 50 ctggktgt 8
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 54 <211> LENGTH: 34
 55 <212> TYPE: PRT
 56 <213> ORGANISM: Homo sapiens
 58 <220> FEATURE:
 59 <223> OTHER INFORMATION: human RAB38 highly conserved N-terminal region
 61 <400> SEQUENCE: 3
 62 Met Gln Ala Pro His Lys Glu His Leu Tyr Lys Leu Leu Val Ile Gly
 63 1 5 10 15

Does Not Comply
 Corrected Diskette Needed
 CP9-S)

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DATE: 11/18/2005

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Input Set : A:\-148-1.app

Output Set: N:\CRF4\11182005\J501611.raw

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68 Asn Phe
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74 <213> ORGANISM: Rattus norvegicus
76 <220> FEATURE:
77 <223> OTHER INFORMATION: rat RAB38 highly conserved N-terminal region
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94 <220> FEATURE:
95 <223> OTHER INFORMATION: mouse RAB38 highly conserved N-terminal region
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104 Asn Phe
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110 <213> ORGANISM: Homo sapiens
112 <220> FEATURE:
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115 <400> SEQUENCE: 6
116 Met Ala Ser Ala Thr Asp Ser Arg Tyr Gly Gln Lys Glu Ser Ser Asp
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132 <223> OTHER INFORMATION: human RAB5 N-terminal region
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Output Set: N:\CRF4\11182005\J501611.raw

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138 Lys Ile Cys Gln Phe Lys Leu Val Leu Leu Gly Glu Ser Ala Val Gly
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148 <213> ORGANISM: Homo sapiens
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151 <223> OTHER INFORMATION: human N-RAS N-terminal region
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158          20          25
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163 <212> TYPE: DNA
164 <213> ORGANISM: Homo sapiens
166 <220> FEATURE:
167 <223> OTHER INFORMATION: Rab38 cDNA
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172 agctgctggt gatcggcgac ctgggtgtgg gcaagaccag cattatcaag cgctatgtgc 180
173 accaaaactt ctctcgcac taccgggcca ccattggtgt ggacttcgcg ctgaagggtgc 240
174 tccactggga cccagagacg gtggtgcgct tgcagctctg ggacattgct ggtcaagaaa 300
175 gatttggaag catgacaaga gtttattacc ggggaagctat gggggcattt attgtttttg 360
176 atgtcaccag accagccaca tttgaagccg tggcaaagtg gaaaaatgat ttggactcaa 420
177 agttaacgct ccctaattgt aagccagtgt cagtgttctt gttggccaac aaatgtgacc 480
178 aagggaagga tgtgcttatg aacaatggac tcaagatgga ccagttctgc aaggagcatg 540
179 gcttcgtagg atggtttgaa acatcagcca aggaaaacat aaacattgat gaagcctcaa 600
180 gatgcctggt caagcacata cttgcaaata agtgtgacct cctagagtct atagaaccgg 660
181 acattgtgaa gccccatctc acatcgccca aggttgtcag ctgctctggc tgtgccaaat 720
182 cctagaaggc tcctctgctg gcatatgaca gacagaacct gtggccctca tgaatcgtgc 780
183 ttcagttttt ccttattacc attttgggta agcgtcagga tagggaagca catgtgacaa 840
184 gccaaagata catgactgta tggttcctgt caaagaggaa cagcaaattg tctttatgtg 900
185 ttttcccacc ccatcagcac agtgtttaca agcttttaaa atattagtct gtcacaatat 960
186 gctgttttat cattgagcaa agccactcag ggacacagac agccctaata tttgttcctt 1020
187 taaatcaaca aaggcttctg gtcttcttga gaaggggaat aacagagcaa ggcagaggtc 1080
188 aagctaagtg tggggatttg tcttgccctg gtgtgtcttt gttcaggtat caatttgttc 1140
189 ccgggtggtc tgataggtct attaaataga aaccattcat ggtagacctt agggttgkct 1200
190 gtgatgtttc tcttcagagt cgtgtgcaca ggcagcctgg gcttttgttg tcacttgctg 1260
191 tgccctgaat gctggtttta ctgaaaactg tatggaaaga tctgctccct gtatgtgcct 1320
192 ttctttcagc ttcctctgac tcaagctgca ggactcttct gtatgtggaa gatattattat 1380
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197 <211> LENGTH: 291
198 <212> TYPE: DNA

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Input Set : A:\-148-1.app

Output Set: N:\CRF4\11182005\J501611.raw

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199 <213> ORGANISM: Homo sapiens
201 <220> FEATURE:
202 <223> OTHER INFORMATION: Rab38 exon 1 and surrounding intron sequence
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205 acatagagct cgggaaacg tcgggtgccc gccccggctg tgcttcccag agcaagctcc 60
206 aggtctccgca agaccgcgg gcctccagga tgcagacacc tcacaaggag cacctgtaca 120
207 agctgctggt gatcggcgac ctgggtgtgg gcaagaccag cattatcaag cgctatgtgc 180
208 accaaaactt ctctcgcac taccgggcca ccattggtgt ggacttcgcg ctgaagggtgc 240
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212 <210> SEQ ID NO: 11
213 <211> LENGTH: 281
214 <212> TYPE: DNA
215 <213> ORGANISM: Homo sapiens
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Rab38 exon 2
220 <400> SEQUENCE: 11
221 gtcaagaaag atttggaac atgacaagag tttattaccg ggaagctatg ggggcattta 60
222 ttgtttttga tgtcaccaga ccagccacat ttgaagccgt ggcaaagtgg aaaaatgatt 120
223 tggactcaaa gttaacgctc cctaattgga agccagtgtc agtggttctg ttggccaaca 180
224 aatgtgacca agggaaggat gtgcttatga acaatggact caagatggac cagttctgca 240
225 aggagcatgg cttcgtagga tggtttgaaa catcagccaa g 281
228 <210> SEQ ID NO: 12
229 <211> LENGTH: 868
230 <212> TYPE: DNA
231 <213> ORGANISM: Homo sapiens
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Rab38 exon 3 and surrounding intron sequence
236 <400> SEQUENCE: 12
237 ggaaaacata aacattgatg aagcctcaag atgcctggtc aagcacatac ttgcaaata 60
238 gtgtgacctc ctagagtcta tagaaccgga cattgtgaag ccccatctca catcgcccaa 120
239 ggttgtcagc tgctctggct gtgccaaatc ctagaaggct cctctgctgg catatgacag 180
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246 tgtgtctttg ttcaggtatc aatttgttcc cgggtggtct gataggctca ttaaatagaa 600
247 accattcatg gtagacctaa gggttgkctg tgatgtttct cttcagagtc gtgtgcacag 660
248 gcagcctggg cttttgttgt cacttgctgt gccctgaatg ctggtttaac tgaaaactgt 720
249 atggaaagat ctgctccctg tatgtgcctt tctttcagct tctctgact caagctgcag 780
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256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Description of Artificial Sequence:TYRP15'T3F

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RAW SEQUENCE LISTING

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Input Set : A:\-148-1.app

Output Set: N:\CRF4\11182005\J501611.raw

262 <400> SEQUENCE: 13
 263 gcgcgaatta accctcacta aagggtctga gcaccctgt cttct
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 292 <212> TYPE: DNA
 293 <213> ORGANISM: Artificial Sequence
 295 <220> FEATURE:
 296 <223> OTHER INFORMATION: Description of Artificial Sequence: MLSN FT3
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 305 <213> ORGANISM: Artificial Sequence
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 308 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR
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 312 taggaaggag gattaaacc g
 315 <210> SEQ ID NO: 18
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 320 <220> FEATURE:
 321 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR
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 328 <210> SEQ ID NO: 19
 329 <211> LENGTH: 26
 330 <212> TYPE: DNA
 331 <213> ORGANISM: Artificial Sequence
 333 <220> FEATURE:

45

45

47

44

21

21

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

Insufficient Response
 What is the source
 of genetic
 material?
 See glen #
 10 on error
 summary
 sheet.

Same
 Error.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/501,611

DATE: 11/18/2005

TIME: 10:51:30

Input Set : A:\-148-1.app

Output Set: N:\CRF4\11182005\J501611.raw